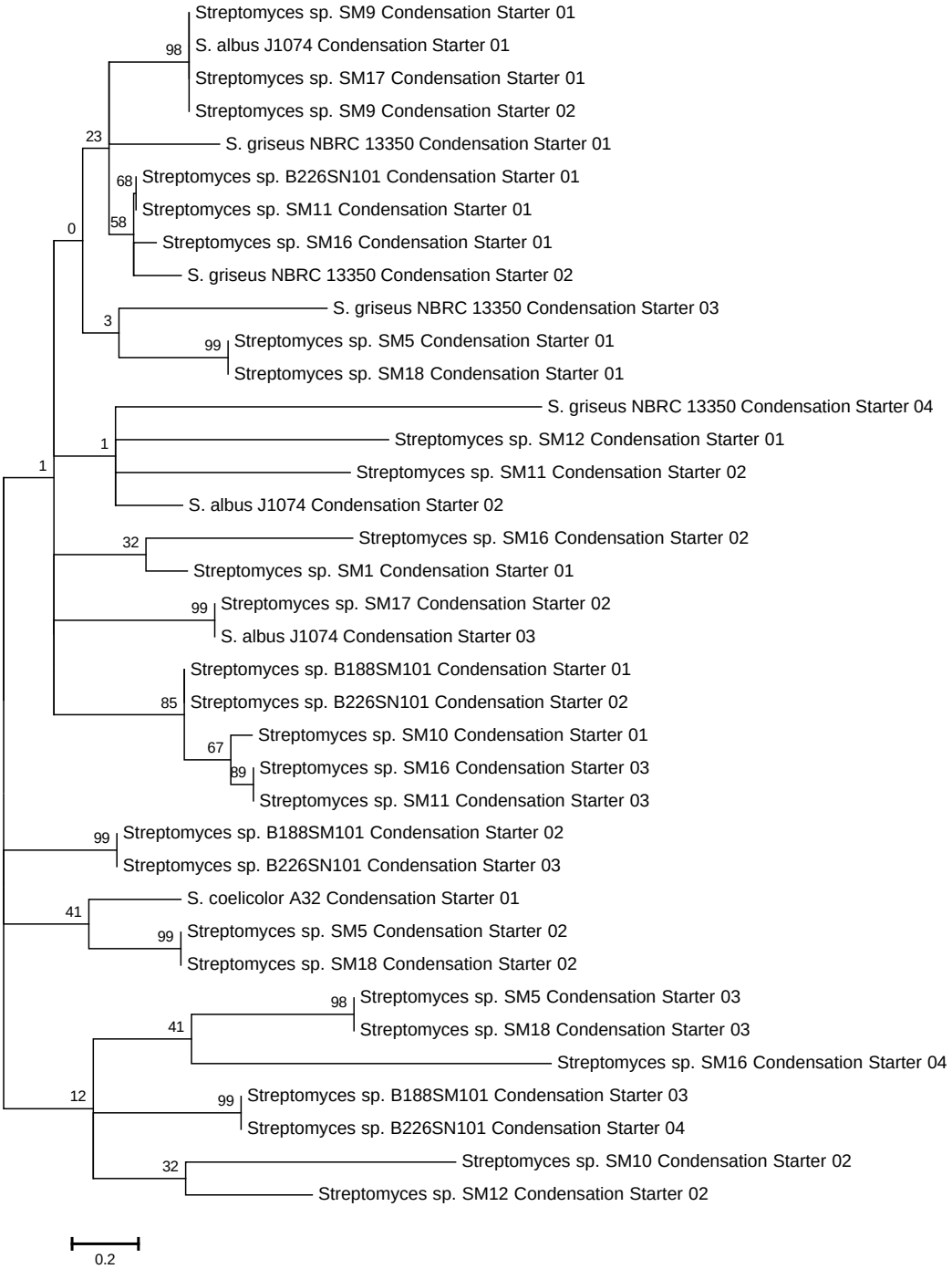
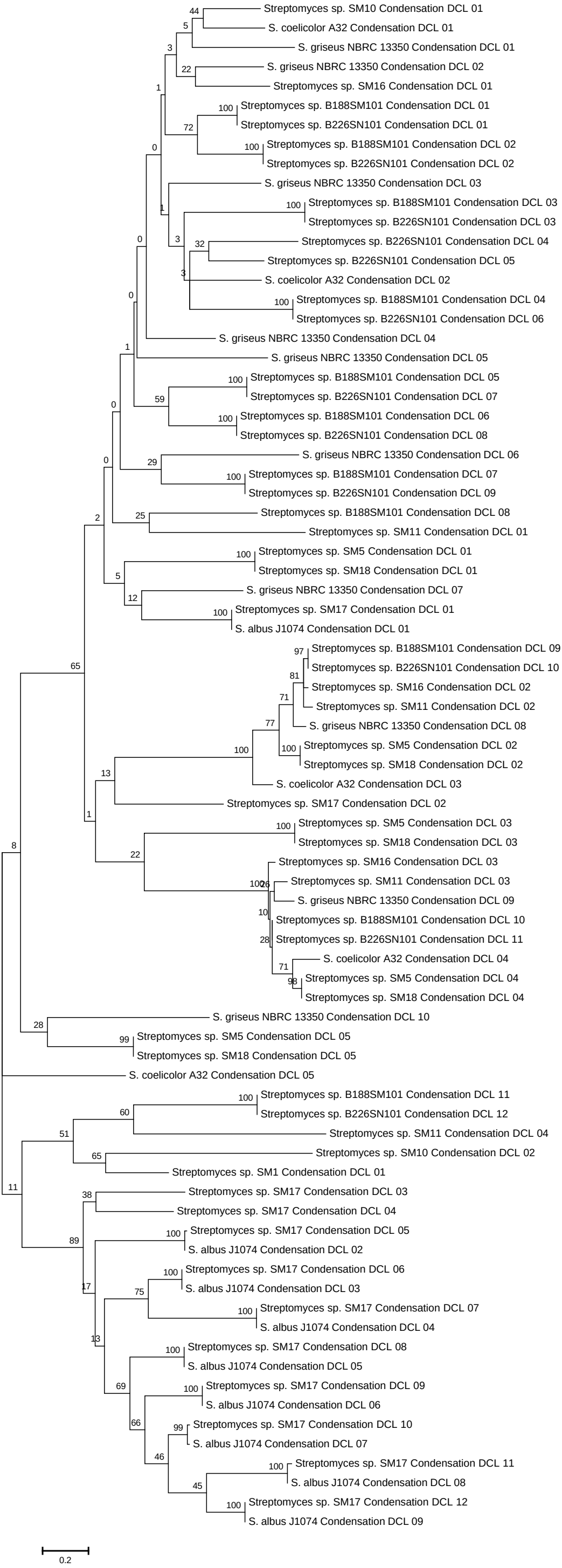
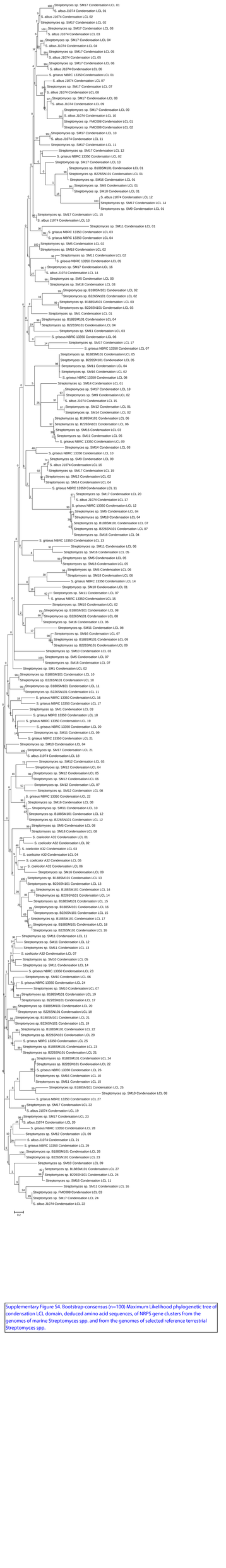
Supplementary Figure S1. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic tree of KS domain, deduced amino acid sequences of PKS gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.



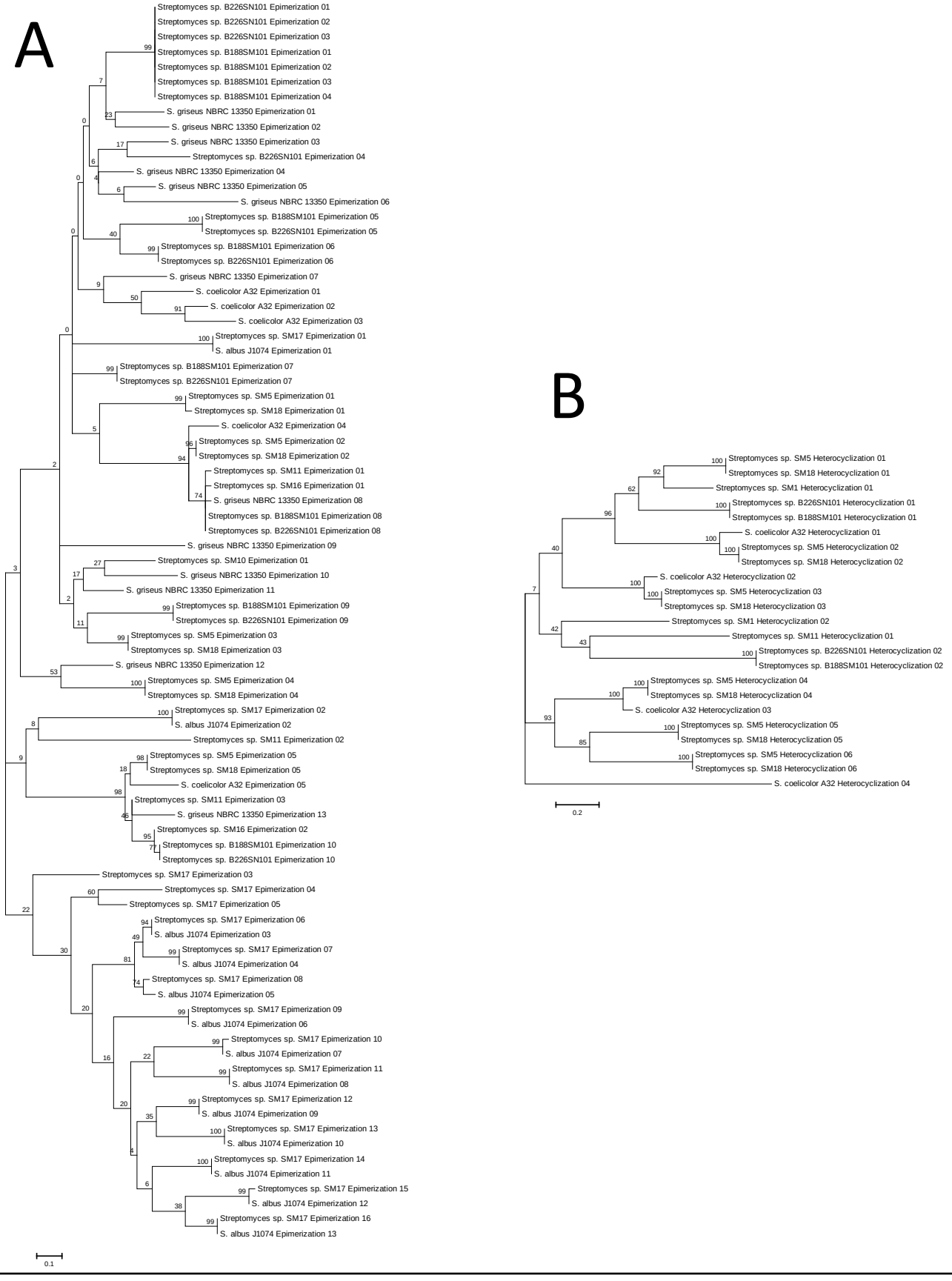

Supplementary Figure S2. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic tree of condensation starter domain, deduced amino acid sequences, of NRPS gene clusters, from the genomes of marine Streptomyces spp. and from the genomes of selected reference terrestrial Streptomyces spp.



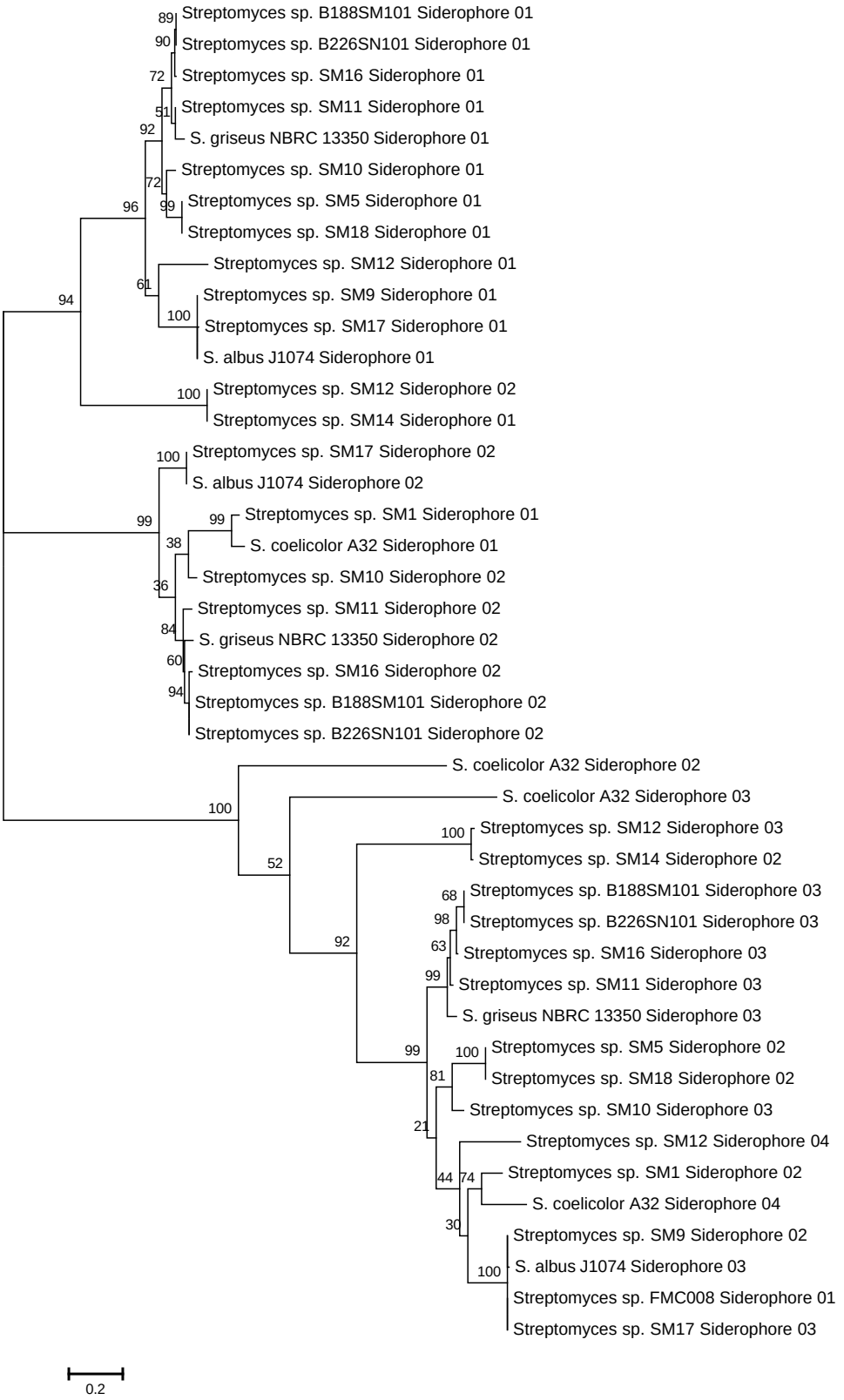

Supplementary Figure S3. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic tree of condensation DCL domain, deduced amino acid sequences, of NRPS gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.



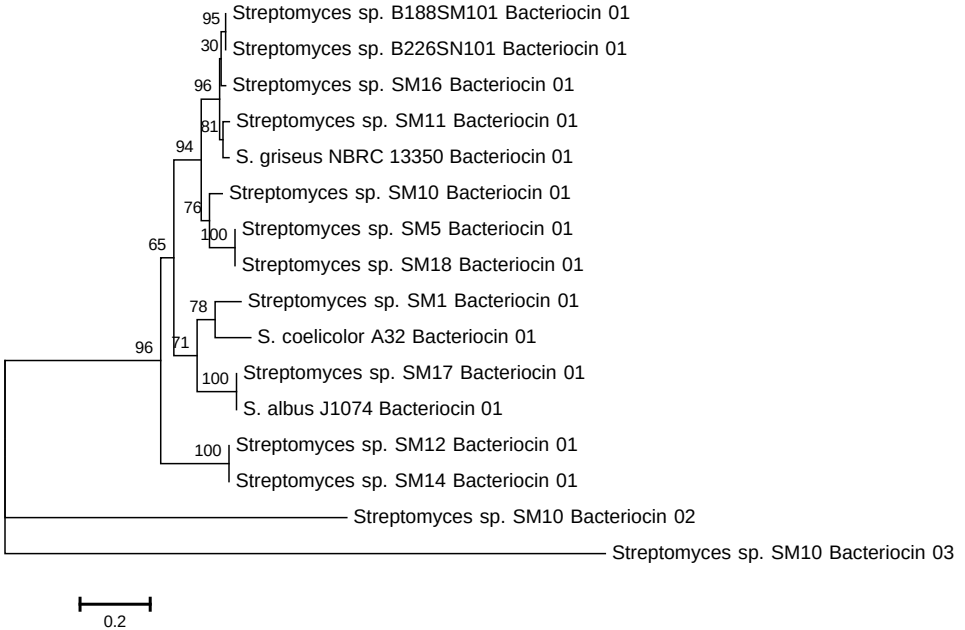

Supplementary Figure S4. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic tree of condensation LCL domains, deduced amino acid sequences, of NRPS-gene clusters from the genomes of marine Streptomyces spp. and from the genomes of selected reference terrestrial Streptomyces spp.



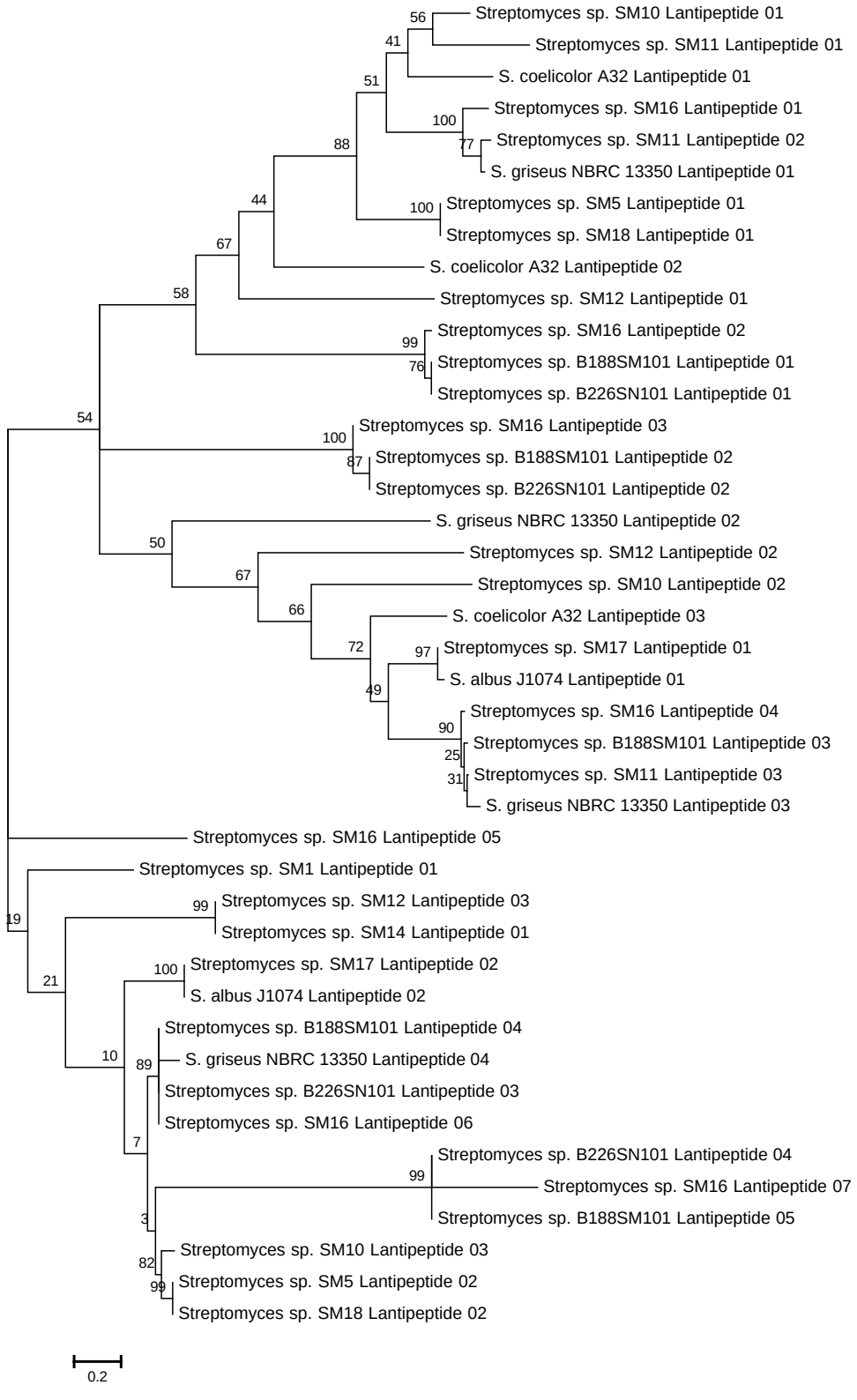

Supplementary Figure S5. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic trees of deduced amino acid sequences of (A) epimerization and (B) heterocyclization domains from NRPS gene clusters, from the genomes of marine Streptomyces spp. and from the genomes of selected reference terrestrial Streptomyces spp.




Supplementary Figure S6. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic trees of deduced amino acid sequences of IucA-IucC domains from siderophore gene clusters, from the genomes of marine Streptomyces spp. and from the genomes of selected reference terrestrial Streptomyces spp.




Supplementary Figure S7. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic trees of deduced amino acid sequences of DUF692 domains from bacteriocin gene clusters, from the genomes of marine Streptomyces spp. and from the genomes of selected reference terrestrial Streptomyces spp.




Supplementary Figure S8. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic trees of deduced amino acid sequences of LanC-like domains from lantipeptide gene clusters, from the genomes of marine Streptomyces spp. and from the genomes of selected reference terrestrial Streptomyces spp.

| Isolate ID | Percentage of sequences assigned to closest sequence in kraken classification with miniKraken database |
|---|---|
| SM1 | 31.7% *Streptomyces coelicolor* A3 (2)<br>18.1% *Streptomyces* root |
| SM5 | 83.91% *Streptomyces sp*. Sirex AA-E |
| SM9 | 97.4% *Streptomyces albus* J1074 |
| SM10 | 55.5% *Streptomyces sp*. Sirex AA-E |
| SM11 | 78.7% *Streptomyces griseus subsp. griseus* NBRC 13350 |
| SM12 | 33.3% *Streptomyces* root<br>47.5% assigned to various *Streptomyces spp*. |
| SM14 | 35.1% *Streptomyces* root<br>47.4% assigned to various *Streptomyces spp*. |
| SM16 | 80.45% *Streptomyces griseus subsp. griseus* NBRC 13350 |
| SM17 | 97.8% *Streptomyces albus* J1074 |
| SM18 | 84.5% *Streptomyces sp*. Sirex AA-E |
| FMC008 | 97.2% *Streptomyces albus* J1074 |
| B188M101 | 82.7% *Streptomyces griseus subsp. griseus* NBRC 13350 |
| B226SN101 | 82.22% *Streptomyces griseus subsp. griseus* NBRC 13350 |

**Supplementary Table S1**. Taxonomy of *Streptomyces* spp. isolates using KRAKEN.

| | B188M101 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | NRPS | Heat Stable Antifungal Factor (HSAF) | 62 |
| 2 | Butyrolactone | Gamma - butyroactone | 100 |
| 3 | Siderophore | Desferrioxamine B | 100 |
| 4 | NRPS-T1PKS | Balhimycin | 8 |
| 5 | NRPS | none | 0 |
| 6 | Lassopeptide | SRO15-2005 | 80 |
| 7 | Others KS | none | 0 |
| 8 | NRPS | Calcium-dependent antibiotic | 5 |
| 9 | Terpene | none | 0 |
| 10 | Ladderane-Arylpoyene | Skyllamycin | 12 |
| 11 | Melanin | Melanin | 100 |
| 12 | Ectoine | Ectoine | 100 |
| 13 | Bacteriocin | none | 0 |
| 14 | Lantipeptide | none | 0 |
| 15 | T3-PKS | Alkylresorcinol | 66 |
| 16 | Bacteriocin | none | 0 |
| 17 | Others-Nrps-T1PKS | Zorbamycin | 4 |
| 18 | T1PKS-NRPS | none | 0 |
| 19 | NRPS | Thaxtomin | 18 |
| 20 | Terpene | none | 0 |
| 21 | Other | none | 0 |
| 22 | T1PKS | SGR-PTMs | 33 |
| 23 | NRPS | none | 0 |
| 24 | T3PKS | Herboxidiene | 6 |
| 25 | NRPS | none | 0 |
| 26 | Terpene | none | 0 |
| 27 | NRPS | Laspartomycin | 6 |
| 28 | NRPS | none | 0 |
| 29 | NRPS | Daptomycin | 18 |
| 30 | Lantipeptide | none | 0 |
| 31 | Phenazine | Lomofungin | 26 |
| 32 | NRPS | none | 0 |
| 33 | NRPS | Friulimicin | 6 |
| 34 | NRPS | Skyllamycin | 16 |
| 35 | Terpene | Hopene | 69 |
| 36 | Siderophore | Kinamycin | 8 |
| 37 | NRPS | Friulimicin | 15 |
| 38 | Butyrolactone | Skyllamycin | 14 |
| 39 | Ectoine | Kosinostatin | 11 |
| 40 | Lantipeptide | AmfS | 60 |
| 41 | NRPS | none | 0 |
| 42 | Thiopeptide-Lantipeptide | none | 0 |
| 43 | NRPS-OthersKS | Kirromycin | 8 |
| 44 | Lassopeptide | Chlortetracycline | 5 |
| 45 | NRPS | Griseobactin | 52 |
| 46 | Lantipeptide | Chalcomycin | 9 |
| 47 | NRPS | none | 0 |
| 48 | Terpene | Isorenieratene | 100 |
| 49 | NRPS | Friulimicin | 18 |
| 50 | NRPS | Coelichelin | 72 |
| 51 | NRPS | Daptomycin | 4 |
| 52 | NRPS | none | 0 |
| 53 | NRPS | none | 0 |

Supplementary Table S2. Secondary metabolism gene cluster types in the draft genome of B188M101, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | B226SN101 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | Bacteriocin | none | 0 |
| 2 | Terpene | none | 0 |
| 3 | Others KS | Eicosapentanoic acid | 33 |
| 4 | Arylpolyene-Ladderene | Skyllamycin | 12 |
| 5 | NRPS-T1PKS | HSAF | 75 |
| 6 | Butyrolactone | Gamma Butyrolactone | 100 |
| 7 | NRPS | none | 0 |
| 8 | Siderophore | Desferrioxamine B | 100 |
| 9 | Melanin | Melanin | 100 |
| 10 | Terpene | none | 0 |
| 11 | NRPS-T1PKS | Zorbamycin | 4 |
| 12 | Ectoine | Kosinostatin | 11 |
| 13 | Lantipeptide | none | 0 |
| 14 | Bacteriocin | none | 0 |
| 15 | T3PKS | Herboxidiene | 6 |
| 16 | Other | none | 0 |
| 17 | NRPS | none | 0 |
| 18 | NRPS | none | 0 |
| 19 | NRPS | none | 0 |
| 20 | Terpene | Hopene | 69 |
| 21 | NRPS | Calcium-dependent antibiotic | 7 |
| 22 | Terpene | none | 0 |
| 23 | NRPS | Friulimicin | 15 |
| 24 | NRPS | none | 0 |
| 25 | Phenazine | Lomofungin | 26 |
| 26 | NRPS | Griseobactin | 29 |
| 27 | Lassopeptide | SRO15-2005 | 60 |
| 28 | Lassopeptide | none | 0 |
| 29 | NRPS | none | 0 |
| 30 | Siderophore | Kinamycin | 8 |
| 31 | NRPS | Daptomycin | 18 |
| 32 | Lantipeptide | none | 0 |
| 33 | NRPS | none | 0 |
| 34 | NRPS | none | 0 |
| 35 | NRPS-T1PKS | Kanamycin | 2 |
| 36 | NRPS | Virginiamycin | 11 |
| 37 | Lantipeptide | Guadinomine | 7 |
| 38 | NRPS | Friulimicin | 15 |
| 39 | NRPS-Others KS | Kirromycin | 8 |
| 40 | Butyrolactone | Skyllamycin | 14 |
| 41 | Ectoine | Ectoine | 100 |
| 42 | Thiopeptide-Lantipeptide | none | 0 |
| 43 | T3PKS | Alkylresorcinol | 100 |
| 44 | NRPS | Grisobactin | 64 |
| 45 | Terpene | Isorenieratene | 100 |
| 46 | NRPS | Coelichelin | 72 |
| 47 | NRPS | none | 0 |
| 48 | NRPS | Daptomycin | 4 |
| 49 | NRPS | WS9326 | 22 |
| 50 | NRPS | Friulimicin | 6 |
| 51 | NRPS | none | 0 |

Supplementary Table S3. Secondary metabolism gene cluster types in the draft genome of B226SN101, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM5 | | |
|---|---|---|---|
| **Cluster no.** | **Cluster type** | **Most similar known cluster** | **% of genes showing similarity** |
| 1 | **Others-T1PKS** | **none** | **0** |
| 2 | **Others-KS** | **none** | **0** |
| 3 | **Terpene** | **Isorenieratene** | **42** |
| 4 | **Other** | **Gobichelin** | **11** |
| 5 | **NRPS** | **Coelichelin** | **72** |
| 6 | **Bacteriocin** | **none** | **0** |
| 7 | **NRPS** | **Coelichelin** | **27** |
| 8 | **NRPS** | **none** | **0** |
| 9 | **Terpene** | **Carbapenem_MM_4550** | **6** |
| 10 | **Terpene** | **Steffimycin** | **11** |
| 11 | **Thiopeptide-Lantipeptide** | **none** | **0** |
| 12 | **NRPS** | **none** | **0** |
| 13 | **Ectoine** | **Ectoine** | **100** |
| 14 | **Others-KS** | **A33853** | **34** |
| 15 | **T1PKS** | **Lasalocid** | **5** |
| 16 | **Butyrolactone** | **Lactonamycin** | **5** |
| 17 | **Terpene** | **none** | **0** |
| 18 | **T1PKS** | **Surfactin** | **8** |
| 19 | **Bacteriocin** | **none** | **0** |
| 20 | **NRPS** | **Mirubactin** | **50** |
| 21 | **Lantipeptide-Lassopeptide** | **none** | **0** |
| 22 | **T1PKS** | **Bafilomycin** | **33** |
| 23 | **NRPS** | **Paenibactin** | **83** |
| 24 | **NRPS-T1PKS** | **Herboxidiene** | **15** |
| 25 | **Siderophore** | **Kinamycin** | **11** |
| 26 | **T1PKS-NRPS** | **Myxothiazol** | **42** |
| 27 | **Melanin** | **Istamycin** | **2** |
| 28 | **NRPS** | **Griseoviridin/Viridogrisien** | **2** |
| 29 | **Terpene** | **Carotenoid** | **27** |
| 30 | **T1PKS** | **Bafilomycin** | **83** |
| 31 | **Other KS** | **none** | **0** |
| 32 | **T2PKS-Terpene** | **Spore Pigment** | **75** |
| 33 | **NRPS** | **Coelibactin** | **90** |
| 34 | **Terpene** | **Hopene** | **69** |
| 35 | **T1PKS** | **Indanomycin** | **17** |
| 36 | **Lantipeptide** | **none** | **0** |
| 37 | **T2PKS-Oligosaccharide** | **Pristinamycin** | **25** |
| 38 | **NRPS** | **SW163** | **28** |

Supplementary Table S4. Secondary metabolism gene cluster types in the draft genome of SM5, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM10 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | Beta-Lactam | Clavams | 35 |
| 2 | Ectoine | Ectoine | 100 |
| 3 | T1PKS | none | 0 |
| 4 | T1PKS | Tetronomycin | 18 |
| 5 | T1PKS | ECO-02301 | 39 |
| 6 | Others-T2PKS | Cinerubin B | 28 |
| 7 | T1PKS | Micromonolactam | 100 |
| 8 | T1PKS | none | 0 |
| 9 | Siderophore | Desferrioxamine B | 83 |
| 10 | Terpene-T2PKS | Spore Pigment | 83 |
| 11 | Melanin | Istamycin | 4 |
| 12 | NRPS | Cystathiazole A | 11 |
| 13 | T3PKS | Tetronasin | 11 |
| 14 | T2PKS | Jadomycin | 100 |
| 15 | Lantipeptide | none | 0 |
| 16 | T1PKS | Lasalocid | 13 |
| 17 | Terpene | none | 0 |
| 18 | Siderophore | none | 0 |
| 19 | Bacteriocin | none | 0 |
| 20 | Butyrolactone | Zorbamycin | 6 |
| 21 | Terpene | Steffinycin | 19 |
| 22 | Lantipeptide | Fluostatin | 4 |
| 23 | T1PKS | none | 0 |
| 24 | T1PKS | none | 0 |
| 25 | Terpene | none | 0 |
| 26 | T1PKS | Sporolide | 21 |
| 27 | Bacteriocin | none | 0 |
| 28 | T1PKS | Aculeximycin | 23 |
| 29 | NRPS | Daptomycin | 9 |
| 30 | Bacteriocin | none | 0 |
| 31 | Thiopeptide | none | 0 |
| 32 | Bacteriocin | none | 0 |
| 33 | T1PKS-Bacteriocin | Hygrocin | 29 |
| 34 | Terpene | Hopene | 76 |
| 35 | Lantipeptide | Ansatrienin (mycotrienin) | 7 |
| 36 | NRPS | Tetronasin | 3 |
| 37 | Butyrolactone | Rabelomycin | 12 |
| 38 | Bacteriocin | none | 0 |
| 39 | Other | Laspartomycin | 11 |
| 40 | Oligosaccharide | none | 0 |
| 41 | T1PKS | Ebelactone | 50 |
| 42 | T1PKS | Thuggacin | 15 |
| 43 | T1PKS | none | 0 |
| 44 | T1PKS | none | 0 |

Supplementary Table S5. Secondary metabolism gene cluster types in the draft genome of SM10, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM11 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | Lassopeptide | none | 0 |
| 2 | NRPS | Coelichelin | 81 |
| 3 | Other | none | 0 |
| 4 | Melanin | Istamycin | 4 |
| 5 | Terpene | Steffimycin | 11 |
| 6 | Other | none | 0 |
| 7 | T1PKS | Bafilomycin | 44 |
| 8 | Lantipeptide | AmfS | 100 |
| 9 | Ectoine | Ectoine | 75 |
| 10 | Thiopeptide-Lantipeptide | none | 0 |
| 11 | NRPS | none | 0 |
| 12 | NRPS | none | 0 |
| 13 | Lantipeptide | none | 0 |
| 14 | T1PKS | Bafilomycin | 83 |
| 15 | T1PKS | Concanamycin A | 21 |
| 16 | NRPS | none | 0 |
| 17 | T3PKS | Alkylresorcinol | 100 |
| 18 | T1PKS | C-1027 | 18 |
| 19 | NRPS | A47934 | 8 |
| 20 | Terpene-Others KS | Pristinamycin | 6 |
| 21 | Ectoine | Kosinostatin | 11 |
| 22 | Butyrolactone | none | 0 |
| 23 | Terpene | Platensimycin/Platencin | 8 |
| 24 | Terpene | Isorenieratene | 100 |
| 25 | T1PKS-NRPS | none | 0 |
| 26 | NRPS | Daptomycin | 7 |
| 27 | T1PKS | SGR-PTMs | 66 |
| 28 | T2PKS | Granaticin | 21 |
| 29 | NRPS | Streptolygidin | 5 |
| 30 | Lantipeptide | none | 0 |
| 31 | Other | none | 0 |
| 32 | NRPS | Tetronasin | 3 |
| 33 | T3PKS | Naringenin | 100 |
| 34 | T1PKS | none | 0 |
| 35 | Other KS | Arsenopolyketides | 20 |
| 36 | NRPS-T1PKS | Herboxidiene | 4 |
| 37 | NRPS | Kirromycin | 28 |
| 38 | Trans AT PKS-NRPS-T1PKS | Kirromycin | 35 |
| 39 | Terpene | none | 0 |
| 40 | Lassopeptide | SRO15-2005 | 80 |
| 41 | Terpene | Hopene | 69 |
| 42 | Melanin | none | 0 |
| 43 | Bacteriocin | none | 0 |
| 44 | Siderophore | Desferrioxamine B | 100 |
| 45 | Siderophore | none | 0 |
| 46 | NRPS | Friulimicin | 21 |
| 47 | Other | Roseoflavin | 100 |
| 48 | NRPS | Griseobactin | 58 |
| 49 | Terpene | none | 0 |
| 50 | Butyrolactone | Gamma Butyrolactone | 100 |
| 51 | NRPS-Bacteriocin | C-1027 | 63 |
| 52 | T2PKS | Chartreusin | 33 |
| 53 | Bacteriocin | none | 0 |
| 54 | Other | Actinomycin | 7 |

Supplementary Table S6. Secondary metabolism gene cluster types in the draft genome of SM11, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM12 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | T1PKS | Stambomycin | 52 |
| 2 | Bacteriocin | none | 0 |
| 3 | T1PKS | none | 0 |
| 4 | T1PKS | none | 0 |
| 5 | T1PKS | Guadinomine | 7 |
| 6 | T1PKS | none | 0 |
| 7 | NRPS | none | 0 |
| 8 | Lantipeptide | none | 0 |
| 9 | Other KS | none | 0 |
| 10 | Oligosaccharide | Pellasoren | 16 |
| 11 | T1PKS | none | 0 |
| 12 | T1PKS | none | 0 |
| 13 | Siderophore | none | 0 |
| 14 | T1PKS | none | 0 |
| 15 | Other KS | none | 0 |
| 16 | NRPS | Laspartomycin | 6 |
| 17 | Lantipeptide | none | 0 |
| 18 | T1PKS | none | 0 |
| 19 | Siderophore | none | 0 |
| 20 | Terpene | none | 0 |
| 21 | T1PKS | none | 0 |
| 22 | Lantipeptide | Kanamycin | 3 |
| 23 | T1PKS | Stambomycin | 60 |
| 24 | T1PKS | Nigericin | 55 |
| 25 | Butyrolactone | none | 0 |
| 26 | NRPS | none | 0 |
| 27 | T1PKS | none | 0 |
| 28 | Ectoine | Ectoine | 100 |
| 29 | T1PKS | Concanamycin | 21 |
| 30 | T3PKS | Zorbamycin | 4 |
| 31 | Siderophore | none | 0 |
| 32 | Siderophore | none | 0 |
| 33 | T1PKS | Sanglifehrin A | 6 |
| 34 | NRPS | Marfomycins | 8 |
| 35 | T1PKS | Thuggacin | 15 |
| 36 | NRPS | none | 0 |
| 37 | NRPS | none | 0 |
| 38 | NRPS | none | 0 |
| 39 | B-Lactam | Clavulanic acid | 20 |
| 40 | T1PKS | Concanamycin A | 28 |

Supplementary Table S7. Secondary metabolism gene cluster types in the draft genome of SM12, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM16 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | Terpene | Steffimycin | 11 |
| 2 | Lantipeptide | AmfS | 40 |
| 3 | Ectoine | Kosinostatin | 9 |
| 4 | Thiopeptide-Lantipeptide | none | 0 |
| 5 | Siderophore | Desferrioxamine B | 100 |
| 6 | NRPS | Oxazolomycin | 6 |
| 7 | Other | none | 0 |
| 8 | T3PKS | Alkylresorcinol | 100 |
| 9 | Terpene | Hopene | 69 |
| 10 | NRPS-T1PKS | Kanamycin | 2 |
| 11 | Bacteriocin-NRPS | Tetronasin | 7 |
| 12 | NRPS-T1PKS | Heat Stable Antifungal Factor (HSAF) | 75 |
| 13 | NRPS | none | 0 |
| 14 | Others KS-NRPS | Bacillibactin | 15 |
| 15 | Lantipeptide | Guadinomine | 7 |
| 16 | Terpene | Glycopeptidolipid | 20 |
| 17 | NRPS-T1PKS-Lantipeptide | none | 0 |
| 18 | Bacteriocin | none | 0 |
| 19 | T3PKS | Herboxidiene | 6 |
| 20 | Lantipeptide | none | 0 |
| 21 | Lassopeptide | SRO15-2015 | 80 |
| 22 | Melanin | Melanin | 100 |
| 23 | Ectoine | Ectoine | 100 |
| 24 | Terpene | none | 0 |
| 25 | Terpene | none | 0 |
| 26 | Terpene | Isorenieratene | 85 |
| 27 | Other KS | Borrelidin | 9 |
| 28 | Other | BE-14106 | 10 |
| 29 | Other KS-T1PKS-Terpene | Isorenieratene | 85 |
| 30 | Lantipeptide | SRO15-2015 | 100 |
| 31 | Lantipeptide | Labyrinthopeptin | 40 |
| 32 | Butyrolactone | Gamma-Butyrolactone | 100 |
| 33 | Terpene | none | 0 |
| 34 | NRPS | Griseobactin | 94 |
| 35 | NRPS | Coelichelin | 81 |
| 36 | Siderophore | Kinamycin | 11 |
| 37 | NRPS | C-1027 | 37 |
| 38 | T1PKS-Butyrolactone | Neocarzinostatin | 52 |
| 39 | NRPS | none | 0 |

Supplementary Table S8. Secondary metabolism gene cluster types in the draft genome of SM16, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM17 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | NRPS | none | 0 |
| 2 | Terpene | none | 0 |
| 3 | NRPS | none | 0 |
| 4 | NRPS | none | 0 |
| 5 | T1PKS | none | 0 |
| 6 | Terpene | Hopene | 46 |
| 7 | Lantipeptide | none | 0 |
| 8 | Bacteriocin | Carotenoid | 18 |
| 9 | NRPS | Mannopeptimycin | 40 |
| 10 | Other | Albachelin | 20 |
| 11 | Lantipeptide | SAL-2242 | 40 |
| 12 | NRPS | none | 0 |
| 13 | NRPS-T1PKS | SGR-PTMs | 10 |
| 14 | NRPS | none | 0 |
| 15 | NRPS | none | 0 |
| 16 | Ectoine | Ectoine | 75 |
| 17 | T1PKS | FR-008 | 71 |
| 18 | Lantipeptide-NRPS-T1PKS | Antimycin | 26 |
| 19 | Siderophore | none | 0 |
| 20 | Bacteriocin | none | 0 |
| 21 | NRPS | none | 0 |
| 22 | Terpene | Albaflavenone | 100 |
| 23 | Terpene | none | 0 |
| 24 | Bacteriocin | none | 0 |
| 25 | T1PKS | none | 0 |
| 26 | T1PKS | none | 0 |
| 27 | T1PKS | none | 0 |
| 28 | T1PKS | Indanomycin | 21 |
| 29 | NRPS | Desotamide | 9 |
| 30 | NRPS | Tertronasin | 9 |
| 31 | Siderophore | Desferrioxamine B | 100 |
| 32 | NRPS | none | 0 |
| 33 | T3PKS | Herboxidiene | 12 |
| 34 | Terpene | none | 0 |
| 35 | T1PKS | none | 0 |
| 36 | NRPS | none | 0 |
| 37 | NRPS | none | 0 |
| 38 | NRPS | none | 0 |
| 39 | NRPS | none | 0 |
| 40 | T1PKS | ECO-02301 | 25 |
| 41 | NRPS | none | 0 |
| 42 | NRPS | none | 0 |
| 43 | T1PKS | none | 0 |
| 44 | T1PKS | none | 0 |
| 45 | T1PKS | none | 0 |
| 46 | Siderophore | none | 0 |
| 47 | T1PKS | Halstoctacosanolide | 77 |
| 48 | NRPS | none | 0 |

Supplementary Table S9. Secondary metabolism gene cluster types in the draft genome of SM17, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM18 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | Butyrolactone | Lactonamycin | 5 |
| 2 | Other KS | A33853 | 34 |
| 3 | NRPS | Coelibactin | 27 |
| 4 | Terpene | Carotenoid | 27 |
| 5 | NRPS | Paenibactin | 66 |
| 6 | Melanin | Melanin | 100 |
| 7 | Lantipeptide | none | 100 |
| 8 | T1PKS | Lasalocid | 5 |
| 9 | Terpene | Steffimycin | 13 |
| 10 | Other KS | none | 0 |
| 11 | T1PKS | Kirromycin | 3 |
| 12 | NRPS | Coelichelin | 27 |
| 13 | NRPS | Coelichelin | 72 |
| 14 | Terpene | Isorenieratene | 57 |
| 15 | T1PKS-NRPS | Cystothiazole A | 17 |
| 16 | NRPS | none | 0 |
| 17 | Other KS-NRPS | SW-163 | 28 |
| 18 | T1PKS | none | 0 |
| 19 | Other KS-T1PKS | none | 0 |
| 20 | NRPS | Mirubactin | 50 |
| 21 | Terpene | none | 0 |
| 22 | Siderophore | none | 0 |
| 23 | Lantipeptide-Lassopeptide | Lipopolysaccharide | 5 |
| 24 | T1PKS | Salinomycin | 18 |
| 25 | Terpene | Hopene | 69 |
| 26 | T1PKS | FD-891 | 62 |
| 27 | NRPS-T1PKS | Herboxidiene | 15 |
| 28 | Oligsaccharide-T2PKS | Granaticin | 43 |
| 29 | Bacteriocin | none | 0 |
| 30 | Bacteriocin | none | 0 |
| 31 | T1PKS | Bafilomycin | 83 |
| 32 | NRPS | none | 0 |
| 33 | Ectoine | Ectoine | 100 |
| 34 | Terpene-T2PKS | Spore Pigment | 75 |
| 35 | Terpene | Carbapenem MM 4550 | 10 |
| 36 | T1PKS | none | 0 |
| 37 | T1PKS | Bafilomycin | 33 |
| 38 | NRPS | Coelibactin | 100 |
| 39 | NRPS | Mannopeptimycin | 7 |
| 40 | T1PKS | none | 0 |
| 41 | Lantipeptide | none | 0 |

Supplementary Table S10. Secondary metabolism gene cluster types in the draft genome of SM18, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM1 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | NRPS | none | 0 |
| 2 | Other KS | none | 0 |
| 3 | NRPS | none | 0 |
| 4 | NRPS | none | 0 |
| 5 | Lantipeptide | none | 0 |
| 6 | NRPS | Erythrochelin | 42 |
| 7 | Siderophore | Desferrioxamine B | 100 |
| 8 | Terpene | none | 0 |
| 9 | Siderophore | Kinamycin | 8 |
| 10 | NRPS | none | 0 |
| 11 | Terpene | Carotenoid | 27 |
| 12 | Lantipeptide | none | 0 |
| 13 | NRPS | none | 0 |
| 14 | T1PKS | Micromonolactam | 100 |
| 15 | T2PKS | Spore Pigment | 83 |
| 16 | Butyrolactone | none | 0 |
| 17 | Terpene | Isorenieratene | 28 |
| 18 | Terpene | Hopene | 15 |
| 19 | Other KS | none | 0 |
| 20 | Terpene | none | 0 |
| 21 | NRPS | none | 0 |
| 22 | Other | none | 0 |
| 23 | Bacteriocin | none | 0 |
| 24 | T1PKS | none | 0 |
| 25 | NRPS | none | 0 |
| 26 | T1PKS-NRPS | Myxalamid | 45 |
| 27 | T1PKS | none | 0 |
| 28 | Bacteriocin | none | 0 |

Supplementary Table S11. Secondary metabolism gene cluster types in the draft genome of SM1, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | FMC008 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | Terpene | none | 0 |
| 2 | Ectoine | Ectoine | 100 |
| 3 | NRPS | Complestatin | 25 |
| 4 | Other | Aureothin | 22 |
| 5 | Terpene | none | 0 |
| 6 | Siderophore | none | 0 |
| 7 | Bacteriocin | none | 0 |
| 8 | T1PKS | none | 0 |
| 9 | Terpene | Phosphonoglycans | 6 |
| 10 | NRPS | Desotamide | 13 |
| 11 | Other | Antimycin | 13 |
| 12 | NRPS | none | 0 |
| 13 | Terpene | none | 0 |
| 14 | Other | none | 0 |
| 15 | Terpene | none | 0 |

Supplementary Table S12. Secondary metabolism gene cluster types in the draft genome of FMC008, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM14 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | T1PKS | none | 0 |
| 2 | T1PKS | none | 0 |
| 3 | B-Lactam | Clavulanic acid | 20 |
| 4 | Siderophore | none | 0 |
| 5 | T1PKS | none | 0 |
| 6 | Lantipeptide | none | 0 |
| 7 | Oligosaccharide | Pellasoren | 16 |
| 8 | T1PKS | none | 0 |
| 9 | T1PKS | Aculeximycin | 23 |
| 10 | T1PKS | none | 0 |
| 11 | NRPS | Calium-dependent antibiotic | 12 |
| 12 | Thiopeptide=Lantipeptide | none | 0 |
| 13 | T3PKS | Zorbamycin | 4 |
| 14 | NRPS | Tetronasin | 3 |
| 15 | T1PKS | none | 0 |
| 16 | Siderophore | none | 0 |
| 17 | Bacteriocin | none | 0 |

Supplementary Table S13. Secondary metabolism gene cluster types in the draft genome of SM14, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

| | SM9 | | |
|---|---|---|---|
| Cluster no. | Cluster type | Most similar known cluster | % of genes showing similarity |
| 1 | Ectoine | Ectoine | 100 |
| 2 | Terpene | none | 0 |
| 3 | Siderophore | none | 0 |
| 4 | NRPS | Antimycin | 20 |
| 5 | T1PKS | Frontalamides | 28 |
| 6 | Terpene | Carotenoid | 18 |
| 7 | Terpene | none | 0 |
| 8 | Bacteriocin | none | 0 |
| 9 | Siderophore | none | 0 |
| 10 | Terpene | none | 0 |
| 11 | Other | none | 0 |
| 12 | Terpene | none | 0 |
| 13 | T1PKS | none | 0 |
| 14 | T1PKS | none | 0 |
| 15 | NRPS | Complestatin | 25 |
| 16 | Terpene | Hopene | 15 |

Supplementary Table S14. Secondary metabolism gene cluster types in the draft genome of SM9, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.